

# Li Tai Fang, Ph.D. (U.S. Citizen)

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## Summary of Accomplishments:

- Expert bioinformatics scientist with extensive experience in cancer informatics
- Authored/co-authored 16 peer-reviewed research articles across multiple disciplines
- Completed the “From The Laboratory To Leadership” program from Leadership Edge
- Invited speaker at 2018 AACR Annual Meeting, 2017 SEQC2 Somatic Mutation Workshop (organized/chaired), 2017 Roche Sequencing Cancer Early Detection Panel, 2016 Roche R&D ExpertFora, 2016 Roche DISRUPT Innovation Mixer, 2016 Bio-IT World Conference

## Professional Experience:

**Roche Sequencing Solutions (Bina Technologies Inc. prior to Dec. 2014)** Belmont, CA  
*Staff Scientist, Bioinformatics (Principal Scientist III)* March, 2018 – Present  
*Senior Scientist, Bioinformatics (Principal Scientist II)* September, 2015 – March, 2018  
*Scientist, Bioinformatics (Principal Scientist I)* March, 2014 – August, 2015

- Lead the SEQC2 subgroup to establish somatic mutation truth set for somatic reference samples
- Represent Roche at the Medical Device Innovation Consortium with regard to somatic reference samples
- Lead developer of SomaticSeq: the machine learning sequencing pipeline (paper is editor’s pick)
- Led Bina Team’s participation in the ICGC-TCGA DREAM Somatic Mutation Calling Challenge: – placed #1 and #2 in Stage 5 of the INDEL and SNV challenges
- Developed key SNV and CNV algorithms incorporated in the Roche’s AVENIO ctDNA RUO product
- Completed somatic SV detection feature set as a part of the \$7.5 million post-acquisition milestone
- Core member of the Roche Sequencing’s Global Career Opportunities and Development Team
- Designed the workflow for the 1000 TCGA Exome re-analysis project on Cancer Genomics Cloud
- Manage data analysis collaboration projects with internal research groups and external customers
- Write white papers, official blogs, peer-reviewed articles, and give live online seminars and talks
- Advocate meticulous documentation practices in the informatics teams using internal wikispaces

**Oxbridge Biotech Roundtable – San Francisco Bay Chapter** San Francisco Bay Area, CA  
*Events Director, Voluntary (25K worldwide and 2,000 local members)* May, 2013 – May, 2014

- Organized roundtable discussions, workshops, and debates on the 1) Commercial potential of big data in biotech, 2) Academic-industry partnerships, 3) Gene patents, 4) Genetically modified food, 5) Science writing, 6) FDA policy on direct-to-consumer genetics test, and 7) Data reproducibility.
- Wrote background articles for promotional purposes, and build rapport with invited speakers
- Recruited 5 mentors for GSK/Roche/McKinsey-sponsored \$150K OneStart Business Plan Competition

**SCIMALS, West Coast Team** San Francisco, CA  
*Investment Analyst, Voluntary* June, 2013 – February, 2014

- Completed a Next Generation Sequencing & Genomic Medicine market analysis project for the venture arm of a hospital network, by leading a team of 5 scientists across different geographical locations
- Prepared project proposals and progress reports, and attended conference calls with venture firms

**UCSF Department of Surgery** San Francisco, CA  
*Bioinformatician, Postdoctoral* March, 2011 – February, 2014

- Implemented the very first Next Generation Sequencing analysis pipeline at Thoracic Oncology Lab
- Co-authored 6 papers, managed a 56-core computing cluster, group website *kimlab.surgery.ucsf.edu*
- Represented and spoke for UCSF Applied Genomics Lab at the 2012 Stanford Lung Cancer Symposium

- Trained lab technicians Linux commands, Bash scripting, computer algorithms, and the tools I created
- Won \$12,500 grant as a team in the “*Idea to IPO 2012*” bioentrepreneurship course sponsored by Burrill & Co., by building a business plan and pitching it to the venture capitalists (2 teams awarded)

### The Hebrew University of Jerusalem

Jerusalem, Israel

*Theoretical Biophysicist, Postdoctoral*

March, 2010 – September, 2010

- Developed and implemented a mathematical model of RNA in 6 months, and published the results
- Discovered and formulated a scaling relationship between RNA’s 3D size and its linear length

### Education:

#### University of California, Los Angeles

Los Angeles, CA

*Ph.D. Biochemistry*

September, 2003 – March, 2010

Had 5 years of hands-on wet lab biochemistry, plus 2+ years of computational/theoretical experience:

- Won the \$1000 Physical Chemistry Research Award as a Biochemistry PhD Student in 2009
- The **only** student in UCLA Biochemistry during my time to publish a **single-authored** research paper
- On my own initiative, developed a mathematical model to calculate the 5’ to 3’ distance of RNA
- Taught 9 classes in Statistical Mechanics, Quantum Mechanics, Thermodynamics, and Biochemistry
- Dissertation: The Physics of DNA, RNA, and RNA-like Polymers
  - ★ Discovered an additional entropic force involved in the release of virus genome
  - ★ Measured the bending and electrostatic energies of DNA in viruses
  - ★ Contributed to the understanding of energies and physical forces inside viruses, relevant to genetic engineering efforts using viruses as delivery vehicles

#### University of California, Berkeley

Berkeley, CA

*B.A. Molecular and Cell Biology*

August, 1999 – May, 2003

- GRE scores: 800 in quantitative; 770 in analytical and logical reasoning (out of 800)
- SAT II scores: 800 in math; 730 in physics

### Selected Publications:

- **Fang LT**, Afshar PT, Chhibber A, *et al.* An ensemble approach to accurately detect somatic mutations using SomaticSeq. *Genome Biol.* 2015;16(1):197. **\*\* Editor’s Pick \*\***
- **Fang LT**, Lee S, Choi H, *et al.* Comprehensive genomic analyses of a metastatic colon cancer to the lung by whole exome sequencing and gene expression analysis. *Int J Oncol.* 2014;44(1):211-21.
- **Fang LT**. The end-to-end distance of RNA as a randomly self-paired polymer. *J Theor Biol.* 2011;280(1):101-7. **\*\* Sole Author \*\***
- **Fang LT**, Gelbart WM, Ben-Shaul A. The size of RNA as an ideal branched polymer. *J Chem Phys.* 2011;135(15):155105.
- **Fang LT**, Yoffe AM, Gelbart WM, Ben-Shaul A. A sequential folding model predicts length-independent secondary structure properties of long ssRNA. *J Phys Chem B.* 2011;115(12):3193-9.

### Non Peer-reviewed:

- SomaticSeq: An ensemble and machine learning approach to accurately detect somatic mutations. *Company Promotional Video*, (12/2015)
- Bina’s official blogs: <http://blog.bina.com/read/author/li-tai-fang>
- Bina Cancer White Paper. *Released in 2014 during ASHG Conference*